Clean Copy of Substitute Specification: the third full paragraph at lines 27 - 28 of page 3

a2 Figure 1B shows the full length DNA sequence of the α subclone of a mhedg-5 pBluescript subclone (SEQ ID NO:22) and the predicted amino acid sequence thereof (SEQ ID NO:23).

Clean Copy of Substitute Specification: the fifth full paragraph at lines 32 - 33 of page 3

a3 Figure 3A shows a nucleotide sequence of hedg-5-cDNA inserted into pcDNA3 (SEQ ID NO:13), nucleotides 36-1097 of which encode the full length HEDG-5. (pC3-hEdg5-3).

Clean Copy of Substitute Specification: the first full paragraph at lines 1 - 2 of page 4

a4 Figure 3B shows a nucleotide sequence of hedg-5 cDNA of clone pC3-hEdg5#3.4 (SEQ ID NO:24), which encodes the full length HEDG-5.

Clean Copy of Substitute Specification: the second full paragraph at lines 4 - 5 of page 4

a5 Figure 3C shows a nucleotide sequence of hedg-5 cDNA of clone pc3-hEdg5#28 (SEQ ID NO:25), which encodes the full length HEDG-5.

Clean Copy of Substitute Specification: the third full paragraph at lines 7 - 9 of page 4

a6 Figure 4A shows an alignment of the genomic DNA (SEQ ID NOS:12, 26) of Figure 3A (which corresponds to the cDNA of the pC3-hEdg5-3 from nt 251-1523 and the genomic DNA flanking from nt 1-250) with the predicted amino acid sequence (SEQ ID NO:14).

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a7 Figure 4B shows the predicted amino acid sequence of hedg-5 cDNA of Figure 3B (SEQ ID NO:27).

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Figure 4C shows the predicted amino acid sequence of hedg-5 cDNA of Figure 3C (SEQ ID NO:28).

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Figure 5A shows the alignment of the predicted amino acid sequences of HEDG5 translation products of clones pC3-hedg5-3, pC3-hedg5#4, and pC3-hedg5#28 as set out in Figures 4A (SEQ ID NO:27), 4B (SEQ ID NO:28) and 4C (SEQ ID NO:28), respectively.

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After surveying various cDNA libraries and first strand cDNA preparations, we were unable to obtain a full-length clone. The rarity of edg-5 in cDNA libraries is further supported by a complete absence of EST's from the edg-5 coding regions in the DBEST database, which contains millions of individual EST's. Therefore, an alternative approach was designed. In this approach, the coding region would be amplified in two fragments from genomic DNA, since we previously determined the location of the single splice site that occurs (between nt 771/772 of SEQUENCE ID NO: 13) in the genomic DNA encoding HEDG5. Then, the two fragments would be joined by an extension PCR in which primers were engineered to contain a 30 bp overlap between the two fragments to obtain a functional, full-length edg5 cDNA, DNA fragments from two exons next to intron located at nt 996/997 were PCR amplified using the following primers so that they have an overlap of 30 nt.

5' Exon Fragment

HE5-261F: [5 '-ATGAATGAGTGTCACTATGACAAG-3'] (SEQ ID NO: 16)

HE5-1011R: [5' -ATACCACAAACGCCCCTAAGACAGTCATCACCGTCTTC-3'] (SEQ ID NO:17)

3' Exon Fragment

a10 cont

HE5-982F: [5'-TGATGACTGTCTTAGGGGCGTTTGTGGTATGCTGGACC-3'] (SEQ ID NO:18)

HE5-1322R: [5'-TTAGGAAGTGCTTTTATTGCAGACTGC-3'] (SEQ ID NO:19)

Clean Copy of Substitute Specification: the second full paragraph at lines 9 - 14 of page 36

To subclone into pcDNA3.1 (Invitrogen; Cat. V795-20) the above DNA was reamplified with modified primers HE5-KZKF and HE5-Kpn1322R under the following conditions:

a11

HE5-KZKF: [5'-TTTAAACTCGAGCCACCATGAATGAGTGTCACTATGAC-3 '] (SEQ ID NO: 20)

HE5-Kpn1322R: [5'-TATATAGGTACCTTAGGAAGTGCTTTTATTGCAGACTGC-3'] (SEQ ID NO: 21)

Clean Copy of Amended Claims

6. (Amended) An isolated nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence comprising nucleotides 36-1907 of SEQ ID NO: 12

(b) the nucleotide sequence of Figure 3B (SEQ ID NO: 24);

(c) the nucleotide sequence of Figure 3C (SEQ ID NO: 25);

a12

(d) the nucleotide sequence comprising at least about 70% sequence identity to (a), (b) or (c) and which hybridizes under stringent conditions to the nucleotide sequence of (a), (b) or (c), respectively; and

(e) the nucleotide sequence which encodes the amino acid sequence of Figure 4A (SEQ ID NO: 14), 4B (SEQ ID NO: 27) or 4C (SEQ ID NO: 28).